

Amendment and Response

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For: SOMATOSTATINS AND METHODS

Please replace the paragraph beginning at **page 12, line 22**, with the following rewritten paragraph. Pursuant to 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

Percent identity is determined by aligning the residues of the two amino acid or nucleotide sequences to optimize the number of identical amino acids or nucleotides along the lengths of their sequences; gaps in either or both sequences are permitted in making the alignment in order to optimize the number of identical amino acids or nucleotides, although the amino acids or nucleotides in each sequence must nonetheless remain in their proper order. Preferably, two amino acid sequences are compared using the Blastp program, version 2.0.9, of the BLAST 2 search algorithm, as described by Tatusova, et al. (*FEMS Microbiol. Lett.*, 174, 247-250 (1999)) and available on the world wide web at www.ncbi.nlm.nih.gov/blast.html. Preferably, the default values for all BLAST 2 search parameters are used, including matrix = BLOSUM62; open gap penalty = 11, extension gap penalty = 1, gap x_dropoff = 50, expect = 10, wordsize = 3, and filter on. Likewise, two nucleotide sequences are compared using the Blastn program, version 2.0.11, of the BLAST 2 search algorithm, also as described by Tatusova, et al. (*FEMS Microbiol Lett*, 174, 247-250 (1999)) and available on the world wide web at www.ncbi.nlm.nih.gov/blast.html. Preferably, the default values for all BLAST 2 search parameters are used, including reward for match = 1, penalty for mismatch = -2, open gap penalty = 5, extension gap penalty = 2, gap x_dropoff = 50, expect = 10, wordsize = 11, and filter on.

Please replace the paragraph beginning at **page 14, line 31**, with the following rewritten paragraph. Pursuant to 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

Further, the single-stranded polynucleotide of the invention also includes a polynucleotide fragment having a nucleotide sequence that is substantially complementary to (a)